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(54) Title: VACCINE COMPOSITIONS COMPRISING LIVE BACTERIAL VECTORS FOR PROTECTION AGAINST YERSINIA PESTIS INJECTION			
(57) Abstract <p>Novel DNA constructs are provided that are capable of transforming microorganisms such that they can be used as live or attenuated vaccines which induce such immune response at mucosal surfaces. Further provided are such transformed microorganisms per se and vaccine compositions containing them. Preferred constructs of the invention are capable of transforming microorganisms such that they express F1 based protein while retaining a capability to establish themselves in human or animal gut environment. Several constructs have been identified that are capable of transforming gut dwelling organisms such as <i>S. typhimurium</i> or <i>S. typhi</i> to enable F1 antigen production, but most of these affect the organism such that it can no longer function effectively in the gut, at least in so far as it cannot express the antigen e.g. being unstable and losing plasmid.</p>			

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VACCINE COMPOSITIONS COMPRISING LIVE BACTERIAL VECTORS FOR PROTECTION AGAINST YERSINIA PESTIS INJECTION.

The present invention relates to novel vaccines for provision of protection against infection with the organism Yersinia pestis (Y. pestis) and to compositions containing them. Particularly provided are parentally and orally active vaccines capable of offering protection against bubonic and pneumonic plague, particularly by induction of mucosal immunity in both humans and other animals.

Y. pestis is the highly virulent causative organism of plague in a wide range of animals, including man. Infection with this organism results in a high rate of mortality. Studies have shown that the high virulence is due to a complex array of factors encoded by both the chromosome and three plasmids, including the Lcr genes (see Straley, (1991) Microb. Pathogen 10: pp87-91), a fibrinolysin (Sodeinde & Goguen, (1988) Infec. Immun 56: pp2743-2748), and a capsule.

The capsule surrounding Y. pestis cells is composed of a protein-polysaccharide complex, the protein component of which is known as Fraction 1 (F1) (see Baker et al (1952) J. Immunol 68: pp131-145) which is only fully expressed at 37°C. This complex confers resistance to phagocytosis, possibly by forming aqueous pores in the membranes of phagocytic cells (Rodrigues et al (1992) J. Med. Biol. Res. 25: pp75-79). Detection of antibodies to F1 is the basis of standard serological tests for the surveillance and diagnosis of plague as infected animals produce a strong humoral response to the antigen (Shepherd et al (1986) J. Clin. Microbiol. 24: pp1075-1078); Williams et al, (1982) Bull. World Health Organ. 64: pp745-752).

The current whole cell vaccines available for prevention of plague are highly heterogeneous, resulting in side effects which make them unsuitable for widespread use (Reisman (1970) J. Allergy 46: pp49-55); Meyer et al (1974) J. Infect. Dis. 129: S13-S18);

Marshall et al (1974) J. Infect. Dis. 129: S19-S25). F1 has been proposed as being the primary immunogen in whole cell vaccines (Williams et al (1980) Bull. World. Health Organ. 58: pp753-756; Chen et al. (1976) J. Infect. Dis. 133: pp302-309) and may therefore be a suitable candidate on which to base an improved vaccine against plague.

The *caf1* gene encoding F1 antigen has been cloned and sequenced (Galyov et al (1990) FEBS Letters 277: pp230-232) and recombinant F1 expressed and purified from *E.coli* induced a protective response in BALB/c mice sufficient to protect against challenge with 10^5 virulent plague bacilli (Simpson et al (1990) Am. J. Trop. Med. Hyg. 43(4): pp389-396). Such resistance to infection by *Y. pestis* is correlated with high titres of F1 antibody.

It is known to orally administer genetically engineered organisms which express antigenic proteins for the purpose of inducing antigen production (EP 0474891) and it is further known that use of such route may result in mucosal immunity (Cardenas & Clements (1992) Clin. Microbiol Rev 5 (3) pp328-342 and (1992) Vaccine 10 (4) pp263). Furthermore, it has been reported that attenuated bacteria have been prepared that are protective against enteric diseases, including genus *Yersinia* (US 6865709).

The current vaccine for plague is the Cutter vaccine which comprises formaldehyde killed plague bacilli and is administered to the body by intramuscular injection. However, parenteral immunisation, although effective in inducing systemic immunity, does not effectively induce mucosal immunity (McGhee et al. (1992) Vaccine 10, 75-88). So far no *Y. pestis* vaccine capable of producing a protective immune response at mucosal surfaces has been developed.

The present inventors have now provided recombinant DNA constructs that when incorporated into DNA of a microorganism, particularly

of a human or animal gut colonising microorganism, are capable of transforming it such that it is able to express a protein which produces a protective immune response against Yersinia pestis in the human or animal body when the gut colonising microorganism is administered by oral routes.

Preferred forms of the present invention provide such DNA constructs that transform such a microorganism while allowing it to maintain its ability to colonise the human or animal gut and thus provide sustained administration, ie. by exposure of antigen to the human or animal body immune system, preferably with systemic invasion of the human or animal body.

Further provided are vectors eg. plasmids, containing the DNA constructs of the invention, that are capable of transforming a human or animal gut colonising microorganism such that it is capable of expressing a protein which produces a protective immune response against Yersinia pestis in a human or animal body when the microorganism is administered by oral or parenteral routes, preferably allowing the microorganism to maintain ability to colonise the human or animal gut, and preferably subsequently systemically to invade the body.

Still further provided are microorganisms, preferably human or animal gut colonising microorganisms, transformed with a vector containing recombinant DNA, eg. a plasmid containing recombinant DNA, according to the invention such that it is enabled to express a protein which produces a protective immune response against Yersinia pestis in a human or animal body when the microorganism is administered by oral or parenteral routes, and preferably allows the microorganism to maintain its ability to colonise the human or animal gut, and preferably invade systemically. The protective response provided preferably includes protection at mucosal surfaces.

One preferred recombinant DNA, and plasmids comprising it, are

characterised in that they comprise a lacZ promoter in frame with a sequence encoding for all or part of the caf1 antigen. Still further preferred recombinant DNA utilises a caf1R positive regulator derived from the F1 operon itself. It is further preferred that the caf1M fragment is included for the purposes of assisting export of mature protein through the cell wall of the host organism, ie. the transformed cell and/or the caf1A fragment that encodes proteins thought to be important in anchoring the F1 subunit to the cell wall.

Where the recombinant DNA includes the lacZ promoter it is preferably incorporated into a vector such as pUC18 that has the all or part of the caf1 encoding sequence inserted in frame with the lacZ promoter

Obviously the microorganisms of the invention are preferably attenuated microorganisms not capable of causing disease in humans or animals, eg. such as the *Salmonella* aro A or aro C mutants, preferably of species *Salmonella typhimurium* or a *Salmonella typhi*. Preferred vaccine compositions are provided as such microorganisms together with a pharmaceutically acceptable carrier, eg. saline or buffer.

Attenuated microorganisms such as *S. typhimurium* have been well characterised as carriers for various heterologous antigens (Curtiss, (1990); New Generation Vaccines, Woodrow & Levine (eds) Marcel Dekker Inc. New York; Cardenas and Clements, (1992) *ibid*). Attenuation may be effected in a number of ways, such as by use of the aro A and/or aro C mutation approach (see Hosie et al (1981) *Nature* 291, 238-239; Dougan et al (1986) *Parasite Immunol* 9, 151-160; Chatfield et al (1989) *Vaccine* 7, 495-498). Many other such attenuating deletions and mutations will be known for these and other microorganisms which will render them suitable for transformation with constructs of the present invention for the purposes of expressing vaccine proteins in the gut and/or gut colonisation in animals to be treated for *Y. pestis*, with systemic invasion and colonisation

following. For human vaccination attenuated S. typhi is the preferred microorganism.

A particularly preferred recombinant DNA, and plasmid or human or animal gut colonising microorganism incorporating it, encodes for or expresses all or part of the mature caf1 (F1) protein of Yersinia pestis. A particularly preferred recombinant DNA comprises a DNA sequence as described in SEQ ID No 4.

The inventors have determined the sequence of a still further preferred recombinant DNA which when included within suitable vectors within, or integrated directly into the chromosomal DNA of, gut dwelling microorganisms results in still stronger expression of protective F1, F1 fusion or F1 truncate proteins. This recombinant DNA is particularly characterised in that it comprises the complete F1 operon including caf1R, a positive regulator of F1 expression; caf1M, encoding for the proposed chaperone sequence which assists in export of the F1 sub-units across the cell wall; caf1A, thought to encode a protein which anchors the F1 into the cell wall; all in addition to the caf1 gene encoding the F1 subunit or a truncate or fusion product thereof.

The method, constructs, microorganisms and vaccines of the invention will now be exemplified by way of illustration only by reference to the following Sequence listing, Figure and Examples. Still further embodiments will be evident to those skilled in the art in the light of these.

SEQUENCE LISTING:

SEQ ID No 1: is the sequence of a PCR primer oligonucleotide corresponding to the first 21 bases encoding for mature caf1 with an additional 5' region encoding for a SacI site.

SEQ ID No 2: is the sequence of a PCR primer oligonucleotide corresponding to the sequence of caf1 which encodes a 'stem loop' downstream of the termination codon with an added 5' region encoding SacI and AccI sites.

SEQ ID No 3: is that of a PCR primer oligonucleotide corresponding to an internal end region of the caf1 gene starting 107 bases downstream from the end of the first oligonucleotide.

SEQ ID No 4: is that of the pFGAL2a construct showing the fusion of the first few bases of the β -galactosidase sequence in the vector with caf1 minus its signal sequence and having a 5' tail including a Sac I restriction site; the sequence is shown up to the caf1 AACC 3' end with some vector bases.

SEQ ID No 5: is that of the protein encoded by pFGAL2a.

SEQ ID No 6: is that of pFSIG3a: including caf1 sequence encoding mature F1 expressed as a fusion with the E. coli LTB signal sequence encoded by the vector and having 5' tail including a SacI restriction site; the sequence shown to AACC at 3' end of caf1 and its adjoining vector bases.

SEQ ID No 7: is that of the protein encoded by pFSIG3a.

SEQ ID No 8: is that of pFORF1b: including the entire caf1 gene and having a 5' tail including a SacI restriction site; the sequence shown to TATAG downstream of the caf1 open reading frame. The two series encoded at the 5' end of the sequence are produced separately to the F1 fusion.

SEQ ID No 9: is that of the end of the first protein encoded by pFORF1b.

SEQ ID No 10: is that of the F1 fusion encoded by pFORF1b.

SEQ ID No 11: is that of primer F1OU2 used to amplify the F1 operon.

SEQ ID No 12: is that of primer M4D used to amplify the F1 operon.

SEQ ID No 13: is that of primer M3U used to amplify the F1 operon.

SEQ ID No 14: is that of primer FIOD2 used to amplify the F1 operon.

SEQ ID No 15: is that of a primer used with the primer of SEQ ID No 1 for preparation of pFSIG3a.

SEQ ID No 16: is that of a primer used with the primer of SEQ ID No 17 to produce pFORF1b.

SEQ ID No 17: is that of a primer used with the primer of SEQ ID No 16 to produce pFORF1b.

FIGURE:

Figure 1 shows schematic representations of the positions of F1 sequences in the constructs pFGAL2a, pFSIG3a and pFORF1b.

Figure 2 shows to relative positions of the primers SEQ ID No 11 to 14, the restriction enzyme sites and the caf1R, caf1M, caf1A and caf1 subunits.

EXAMPLES.

General methods: Y. pestis was grown aerobically at 28°C in Blood Agar Base broth, pH6.8, containing 15g/l proteose peptone, 2.5g/l liver digest, 5g/l yeast extract, 5g/l NaCl supplemented with 80ml 0.25% haemin in 1/100N NaOH. Strains of S. typhimurium used were

SL3261 and LB5010 as described by Hosieth & Stocker (1981) Nature (London) 291: p238-239 and Maskell et al (1987) Microb. Pathog. 2 pp211-221 respectively and these and E.coli JM109 were cultured and stored as described by Sambrook et al (1989) Molecular Cloning Manual.

Cloning of caf1: DNA was isolated from Y. pestis by the method of Marmur et al (1961) J. Mol. Biol. 3: pp 208-218. A DNA fragment encoding the open reading frame of caf1 minus its signal sequence was amplified from this using the polymerase chain reaction (PCR).

Oligonucleotides were prepared with a Beckman 200A DNA synthesiser for use in the PCR.

EXAMPLE 1: pFGAL2a construct:

Oligonucleotide GATCGAGCTCGGCAGATTAACTGCAAGCACC (SEQ ID No 1) was synthesised corresponding to the first 21 bases of caf1 immediately following the nucleotides encoding the signal sequence with an additional 5' region encoding a SacI site and the complimentary oligonucleotide CAGGTCGAGCTCGTCGACGGTTAGGCTCAAAGTAG (SEQ ID No 2) corresponding to the sequence which encodes a putative 'stem loop' structure downstream of the caf1 termination codon with an added 5' region encoding SacI and AccI sites. A DNA fragment was obtained after 35 cycles of amplification (95°C, 15 secs; 50°C, 15 secs; 72°C, 30 secs using a Perkin Elmer 9600 GeneAmp PCR system). The fragment was purified, digested with SacI and AccI, ligated into a similarly digested pUC18 plasmid and transformed into E. coli JM109 by electroporation. Electroporation was carried out using a Biorad Gene Pulser with 0.2 cm cuvettes at 1.25kV, 25µF, 8000hms with a time constant of 20.

A pFGAL2a colony containing the cloned caf1 gene was identified by PCR using an oligonucleotide TGGTACGCTTACTCTTGGCGGCTAT (SEQ ID No 3) corresponding to an internal region of the gene 128 to 153 nucleotides from the site identified as the signal sequence cleavage site (see

Galyov et al (1990)) and the SEQ ID No 2. A culture of the *E.coli* containing the pFGAL2a was grown at 37°C with shaking in Luria Broth containing 1mM isopropyl-β-D-thiogalactopyranoside (IPTG) for 18 hours. Whole cell lysates and periplasmic and cytoplasmic fractions of the bacteria were prepared as described by Sambrook et al (1989).

SDS-PAGE and Western blotting: SDS-polyacrylamide gel electrophoresis (PAGE) and Western blotting were performed as described by Hunter et al (1993) *Infect. Immun.* 61. 3958-3965. Blots were probed with polyclonal antisera raised in sheep (B283) against killed *Y. pestis* (EV76 strain grown at 37°C) and bound antibody was detected with a horseradish peroxidase-labelled donkey anti-sheep IgG (Sigma).

Expression of F1 in *S. typhimurium*: The pFGAL2a plasmid was isolated using general techniques described in Sambrook et al (1989) *Molecular Cloning; a Laboratory Manual*. 2nd Edition. Cold Spring Harbour Laboratory, New York. Purified plasmid was electroporated into *S. typhimurium* LB5010 (restriction⁻, modification⁻) and methylated pFGAL2a was subsequently isolated from the LB5010 for electroporation into *S. typhimurium* SL3261 (aro A⁻). Periplasmic and cytoplasmic fractions were prepared for SDS-PAGE and Western blotting as described above.

Stability of constructs: Five female Balb/c mice were inoculated intravenously with either 5x10⁵ or 5x10⁷ cfu *S. typhimurium* containing pFGAL2a in 200μl phosphate buffered saline. Control mice were inoculated similarly with *S. typhimurium* containing pUC18 with no insert. After 7 days the mice were killed by cervical dislocation and their livers and spleens removed. The organs were homogenised in 10ml phosphate buffered saline using a stomacher on maximum setting for 2 minutes and the homogenate was serially diluted in phosphate buffered saline and placed onto L agar or L agar containing 55μg ml⁻¹ ampicillin.

Challenge of immunized mice: Male Balb/c mice were inoculated with three doses of *S.typhimurium* containing pFGAL2a, intravenously (i.v.) with 5×10^7 cfu bacteria at 7 day intervals, or intragastrically (i.g.) by intubation with 1×10^{10} cfu on days 1, 7 and 21. Ampicillin was given subcutaneously for 5 days after each inoculation to stabilise the plasmid. Six weeks after the last dose five mice from both the i.g. and intravenously inoculated groups were bled then killed by cervical dislocation and their livers and spleens taken. Livers were homogenised and plated onto L-agar to confirm that all *Salmonella* had been cleared.

The remaining mice were challenged subcutaneously with $50LD_{50}$ of *Y. pestis* strain GB. Control mice were immunised i.v. and i.g. with *S. typhimurium* containing pUC18, intramuscularly with formaldehyde-killed plague vaccine (Cutter USP) or intraperitoneally with 10µg of purified F1 and survival rates assessed (see Table 1).

EXAMPLE 2: pFSIG3a construct:

Construct plasmids and *S. typhimurium* transformed by them were obtained using the method of Example 1 altered in so far as the PCR product was designed to be of SEQ ID No 2 after digestion with SacI. The digested product was ligated into SacI digested pFS2.2 giving the sequence SEQ ID No 5 located as shown in Figure I. This construct encodes for F1 which is expressed as a fusion with the *E.coli* LTB signal sequence. The primer used instead of SEQ ID No 1 was that of SEQ ID No 15.

Example 3: pFORF1b construct:

Construct plasmids and *S. typhimurium* transformed by them were obtained using the method of Example 1 altered in so far as the PCR primers were selected to produce an amplification product which after digestion with SacI/AccI consisted of SEQ ID No 6.

Primers used were of sequences SEQ ID NO 16 and SEQ ID No 17.

This construct incorporates the *caf1* signal sequence in addition the mature protein sequence as shown in SEQ ID No 6 and Fig 1 which shows all bases downstream of the *Sac* I site used for digest.

Protection provided by intravenous injection and oral delivery of *S.typhimurium* transformed with plasmids containing various constructs of the invention and comparative protection afforded by direct administration of F1 and Cutter vaccines. *S. typhimurium* transformed as described above with either pFGAL2a, pFSIG3a, pFORF1b or unmodified pUC18 were administered to mice by intravenous or intragastric routes and compared in effect to intraperitoneal F1 and intramuscular Cutter vaccine as described above in Example 1.

TABLE 1. CHALLENGE OF MICE WITH 50 x MICE LD ₅₀ Y. PESTIS			
IV or IM*TREATMENT	SURVIVORS	ORAL TREATMENT	SURVIVORS
<i>S.typhimurium</i> /pFSIG3a IV	10/10	<i>S.typhimurium</i> /pFSIG3a	1/10
<i>S.typhimurium</i> /pFGAL2a IV	9/10	<i>S.typhimurium</i> /pFGAL2a	9/10
<i>S.typhimurium</i> /pFORF1b IV	10/10	<i>S.typhimurium</i> /pFORF1b	3/10
<i>S.typhimurium</i> /pUC18 IV	0/10	<i>S.typhimurium</i> /pUC18	0/5
F1 protein IP	6/8		
Cutter vaccine IM	9/10		

IV = intravenous IM = intramuscular IP = intraperitoneally

EXAMPLE 4: F1 operon construct:

Attempts to PCR replicate the entire F1 operon as one piece were unsuccessful, so a strategy was developed whereby it was amplified using PCR to produce two discrete fragments using primer pairs (A) of SEQ ID No 11 and 12 and (b) of SEQ No 13 and 14 respectively to produce fragments of 3.36kb and 1.89kb from Y. pestis MP6 template DNA. Marmur extract of DNA was used without CsCl₂ purification. The PCR cycle conditions used were 96°C for 30 seconds, 57°C for 30 seconds and 72°C for 1 minute; total of 30 cycles.

These two fragments were digested using NheI and joined together. This fused fragment, encoding the full length operon (5.25kb), was digested with EcoRI and SalI and then cloned into a number of vectors. When this fragment was cloned into pBR322 and expressed in E. coli, S. typhimurium LB5010 or SL3261 instability of the recombinant plasmid was noted. To circumvent this problem the operon was cloned into plasmid pLG339, a low copy number plasmid km^R. The entire F1 operon was also been inserted into AroC gene on the chromosome of S. typhimurium using vector pBRD1084.

The positions of the primers, restriction sites and caf1R to caf1 are shown in Figure 2.

Full protection (4/4) of mice challenged with with 10⁴ lethal doses of Y. pestis was provided on administration of these transformed organisms.

SEQUENCE LISTING

1) GENERAL INFORMATION:

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(F) POSTAL CODE (ZIP): SP4 OJQ

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- (ii) TITLE OF INVENTION: VACCINE COMPOSITIONS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release @1.0, Version @1.25 (EPO)
- (vi) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: GB 9326425.7
 - (B) FILING DATE: 24-DEC-1993

- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Yersinia pestis
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GATCGAGCTC GGCAGATTTA ACTGCAAGCA CC

32

- (2) INFORMATION FOR SEQ ID NO: 2:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Yersinia pestis
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

CAGGTCGAGC TCGTCGACGG TTAGGCTCAA AGTAG

35

- (2) INFORMATION FOR SEQ ID NO: 3:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOTHETICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Yersinia pestis
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

TGGTACGCTT ACTCTTGGCG GCTAT

25

15

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A)LENGTH: 541 base pairs

(B)TYPE: nucleic acid

(C)STRANDEDNESS: double

(D)TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii)HYPOTHETICAL: NO

(iii)ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A)ORGANISM: *Yersinia.pestis*

(ix) FEATURE:

(A)NAME/KEY: CDS

(B)LOCATION: 2..454

(ix) FEATURE:

(A)NAME/KEY: misc recomb

(B)LOCATION: 1..6

(ix) FEATURE:

(A)NAME/KEY: misc_recomb

(B)LOCATION: 536..541

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

G AGC TCG GCA GAT TTA ACT GCA AGC ACC ACT GCA ACG GCA ACT CTT	46
Ser Ser Ala Asp Leu Thr Ala Ser Thr Thr Ala Thr Ala Thr Leu	
1 5 10 15	
GTT GAA CCA GCC CGC ATC ACT ATT ACA TAT AAG GAA GGC GCT CCA ATT	94
Val Glu Pro Ala Arg Ile Thr Ile Thr Tyr Lys Glu Gly Ala Pro Ile	
20 25 30	
ACA ATT ATG GAC AAT GGA AAC ATC GAT ACA GAA TTA CTT GTT GGT ACG	142
Thr Ile Met Asp Asn Gly Asn Ile Asp Thr Glu Leu Leu Val Gly Thr	
35 40 45	
CTT ACT CTT GGC GGC TAT AAA ACA GGA ACC ACT AGC ACA TCT GTT AAC	190
Leu Thr Leu Gly Gly Tyr Lys Thr Gly Thr Thr Ser Thr Ser Val Asn	
50 55 60	
TTT ACA GAT GCC GCG GGT GAT CCC ATG TAC TTA ACA TTT ACT TCT CAG	238
Phe Thr Asp Ala Ala Gly Asp Pro Met Tyr Leu Thr Phe Thr Ser Gln	
65 70 75	
GAT GGA AAT AAC CAC CAA TTC ACT ACA AAA GTG ATT GGC AAG GAT TCT	286
Asp Gly Asn Asn His Gln Phe Thr Thr Lys Val Ile Gly Lys Asp Ser	
80 85 90 95	
AGA GAT TTT GAT ATC TCT CCT AAG GTA AAC GGT GAG AAC CTT GTG GGG	334
Arg Asp Phe Asp Ile Ser Pro Lys Val Asn Gly Glu Asn Leu Val Gly	
100 105 110	
GAT GAC GTC GTC TTG GCT ACG GGC AGC CAG GAT TTC TTT GTT CGC TCA	382
Asp Asp Val Val Leu Ala Thr Gly Ser Gln Asp Phe Phe Val Arg Ser	
115 120 125	

16

ATT GGT TCC AAA GGC GGT AAA CTT GCA GCA GGT AAA TAC ACT GAT GCT 430
 Ile Gly Ser Lys Gly Gly Lys Leu Ala Ala Gly Lys Tyr Thr Asp Ala
 130 135 140

GTA ACC GTA ACC GTA TCT AAC CAA TAATCCATAT AGATAATAGA TAAAGGAGGG 484
 Val Thr Val Thr Val Ser Asn Gln
 145 150

CTATTATGCC CTCCTTTAAT ATTTATGAAT TATCCTACTT TGAGCCTAAC CGTCGAC 541

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Ser Ser Ala Asp Leu Thr Ala Ser Thr Thr Ala Thr Ala Thr Leu Val
 1 5 10 15
 Glu Pro Ala Arg Ile Thr Ile Thr Tyr Lys Glu Gly Ala Pro Ile Thr
 20 25 30
 Ile Met Asp Asn Gly Asn Ile Asp Thr Glu Leu Leu Val Gly Thr Leu
 35 40 45
 Thr Leu Gly Gly Tyr Lys Thr Gly Thr Thr Ser Thr Ser Val Asn Phe
 50 55 60
 Thr Asp Ala Ala Gly Asp Pro Met Tyr Leu Thr Phe Thr Ser Gln Asp
 65 70 75 80
 Gly Asn Asn His Gln Phe Thr Thr Lys Val Ile Gly Lys Asp Ser Arg
 85 90 95
 Asp Phe Asp Ile Ser Pro Lys Val Asn Gly Glu Asn Leu Val Gly Asp
 100 105 110
 Asp Val Val Leu Ala Thr Gly Ser Gln Asp Phe Phe Val Arg Ser Ile
 115 120 125
 Gly Ser Lys Gly Gly Lys Leu Ala Ala Gly Lys Tyr Thr Asp Ala Val
 130 135 140
 Thr Val Thr Val Ser Asn Gln
 145 150

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)
 (iii) HYPOTHETICAL: NO
 (iii) ANTI-SENSE: NO
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia pestis*
 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 3..455
 (ix) FEATURE:
 (A) NAME/KEY: misc_recomb
 (B) LOCATION: 1..6
 (ix) FEATURE:
 (A) NAME/KEY: misc_recomb
 (B) LOCATION: 536..541
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

GA GCT CCC GCA GAT TTA ACT GCA AGC ACC ACT GCA ACG GCA ACT CTT 47
Ala Pro Ala Asp Leu Thr Ala Ser Thr Thr Ala Thr Leu
  1             5             10             15

GTT GAA CCA GCC CGC ATC ACT ATT ACA TAT AAG GAA GGC GCT CCA ATT 95
Val Glu Pro Ala Arg Ile Thr Ile Thr Tyr Lys Glu Gly Ala Pro Ile
              20             25             30

ACA ATT ATG GAC AAT GGA AAC ATC GAT ACA GAA TTA CTT GTT GGT ACG 143
Thr Ile Met Asp Asn Gly Asn Ile Asp Thr Glu Leu Leu Val Gly Thr
              35             40             45

CTT ACT CTT GGC GGC TAT AAA ACA GGA ACC ACT AGC ACA TCT GTT AAC 191
Leu Thr Leu Gly Gly Tyr Lys Thr Gly Thr Thr Ser Thr Ser Val Asn
              50             55             60

TTT ACA GAT GCC GCG GGT GAT CCC ATG TAC TTA ACA TTT ACT TCT CAG 239
Phe Thr Asp Ala Ala Gly Asp Pro Met Tyr Leu Thr Phe Thr Ser Gln
              65             70             75

GAT GGA AAT AAC CAC CAA TTC ACT ACA AAA GTG ATT GGC AAG GAT TCT 287
Asp Gly Asn Asn His Gln Phe Thr Thr Lys Val Ile Gly Lys Asp Ser
              80             85             90             95

AGA GAT TTT GAT ATC TCT CCT AAG GTA AAC GGT GAG AAC CTT GTG GGG 335
Arg Asp Phe Asp Ile Ser Pro Lys Val Asn Gly Glu Asn Leu Val Gly
              100            105            110

GAT GAC GTC GTC TTG GCT ACG GGC AGC CAG GAT TTC TTT GTT CGC TCA 383
Asp Asp Val Val Leu Ala Thr Gly Ser Gln Asp Phe Phe Val Arg Ser
              115            120            125

ATT GGT TCC AAA GGC GGT AAA CTT GCA GCA GGT AAA TAC ACT GAT GCT 431
Ile Gly Ser Lys Gly Gly Lys Leu Ala Ala Gly Lys Tyr Thr Asp Ala
              130            135            140

GTA ACC GTA ACC GTA TCT AAC CAA TAATCCATA TAGATAATAG ATAAAGGAGG 484
Val Thr Val Thr Val Ser Asn Gln
              145            150

```

GCTATTATGC CCTCCTTTAA TATTTATGAA TTATCCTACT TTGAGCCTAA CCGTCGAC 542

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Ala	Pro	Ala	Asp	Leu	Thr	Ala	Ser	Thr	Thr	Ala	Thr	Ala	Thr	Leu	Val	1	5	10	15
Glu	Pro	Ala	Arg	Ile	Thr	Ile	Thr	Tyr	Lys	Glu	Gly	Ala	Pro	Ile	Thr	20	25	30	
Ile	Met	Asp	Asn	Gly	Asn	Ile	Asp	Thr	Glu	Leu	Leu	Val	Gly	Thr	Leu	35	40	45	
Thr	Leu	Gly	Gly	Tyr	Lys	Thr	Gly	Thr	Thr	Ser	Thr	Ser	Val	Asn	Phe	50	55	60	
Thr	Asp	Ala	Ala	Gly	Asp	Pro	Met	Tyr	Leu	Thr	Phe	Thr	Ser	Gln	Asp	65	70	75	80
Gly	Asn	Asn	His	Gln	Phe	Thr	Thr	Lys	Val	Ile	Gly	Lys	Asp	Ser	Arg	85	90	95	
Asp	Phe	Asp	Ile	Ser	Pro	Lys	Val	Asn	Gly	Glu	Asn	Leu	Val	Gly	Asp	100	105	110	
Asp	Val	Val	Leu	Ala	Thr	Gly	Ser	Gln	Asp	Phe	Phe	Val	Arg	Ser	Ile	115	120	125	
Gly	Ser	Lys	Gly	Gly	Lys	Leu	Ala	Ala	Gly	Lys	Tyr	Thr	Asp	Ala	Val	130	135	140	
Thr	Val	Thr	Val	Ser	Asn	Glu	145	150											

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 542 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Yersinia pestis*

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..7

(ix) FEATURE:

(A) NAME/KEY: misc_recomb

(B) LOCATION: 1..6

(ix) FEATURE:

(A) NAME/KEY: misc_recomb

(B) LOCATION: 536..541

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 21..530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

G AGC TCG TAGGAGGTAA TAT ATG AAA AAA ATC AGT TCC GTT ATC GCC ATT 50
 Ser Ser Met Lys Lys Ile Ser Ser Val Ile Ala Ile
 1 1 5 10

GCA TTA TTT GGA ACT ATT GCA ACT GCT AAT GCG GCA GAT TTA ACT GCA 98
 Ala Leu Phe Gly Thr Ile Ala Thr Ala Asn Ala Ala Asp Leu Thr Ala
 15 20 25

AGC ACC ACT GCA ACG GCA ACT CTT GTT GAA CCA GCC CGC ATC ACT CTT 146
 Ser Thr Thr Ala Thr Ala Thr Leu Val Glu Pro Ala Arg Ile Thr Leu
 30 35 40

ACA TAT AAG GAA GGC GCT CCA ATT ACA ATT ATG GAC AAT GGA AAC ATC 194
 Thr Tyr Lys Glu Gly Ala Pro Ile Thr Ile Met Asp Asn Gly Asn Ile
 45 50 55

GAT ACA GAA TTA CTT GTT GGT ACG CTT ACT CTT GGC GGC TAT AAA ACA 242
 Asp Thr Glu Leu Leu Val Gly Thr Leu Thr Leu Gly Gly Tyr Lys Thr
 60 65 70

GGA ACC ACT AGC ACA TCT GTT AAC TTT ACA GAT GCC GCG GGT GAT CCC 290
 Gly Thr Thr Ser Thr Ser Val Asn Phe Thr Asp Ala Ala Gly Asp Pro
 75 80 85 90

ATG TAC TTA ACA TTT ACT TCT CAG GAT GGA AAT AAC CAC CAA TTC ACT 338
 Met Tyr Leu Thr Phe Thr Ser Gln Asp Gly Asn Asn His Gln Phe Thr
 95 100 105

ACA AAA GTG ATT GGC AAG GAT TCT AGA GAT TTT GAT ATC TCT CCT AAG 386
 Thr Lys Val Ile Gly Lys Asp Ser Arg Asp Phe Asp Ile Ser Pro Lys
 110 115 120

GTA AAC GGT GAG AAC CTT GTG GGG GAT GAC GTC GTC TTG GCT ACG GGC 434
 Val Asn Gly Glu Asn Leu Val Gly Asp Asp Val Val Leu Ala Thr Gly
 125 130 135

AGC CAG GAT TTC TTT GTT CGC TCA ATT GGT TCC AAA GGC GGT AAA CTT 482
 Ser Gln Asp Phe Phe Val Arg Ser Ile Gly Ser Lys Gly Gly Lys Leu
 140 145 150

GCA GCA GGT AAA TAC ACT GAT GCT GTA ACC GTA ACC GTA TCT AAC CAA 530
 Ala Ala Gly Lys Tyr Thr Asp Ala Val Thr Val Thr Val Ser Asn Gln
 155 160 165 170

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542

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Ser Ser

1

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Met Lys Lys Ile Ser Ser Val Ile Ala Ile Ala Leu Phe Gly Thr Ile
 1 5 10 15

Ala Thr Ala Asn Ala Ala Asp Leu Thr Ala Ser Thr Thr Ala Thr Ala
 20 25 30

Thr Leu Val Glu Pro Ala Arg Ile Thr Leu Thr Tyr Lys Glu Gly Ala
 35 40 45

Pro Ile Thr Ile Met Asp Asn Gly Asn Ile Asp Thr Glu Leu Leu Val
 50 55 60

Gly Thr Leu Thr Leu Gly Gly Tyr Lys Thr Gly Thr Thr Ser Thr Ser
 65 70 75 80

Val Asn Phe Thr Asp Ala Ala Gly Asp Pro Met Tyr Leu Thr Phe Thr
 85 90 95

Ser Gln Asp Gly Asn Asn His Gln Phe Thr Thr Lys Val Ile Gly Lys
 100 105 110

Asp Ser Arg Asp Phe Asp Ile Ser Pro Lys Val Asn Gly Glu Asn Leu
 115 120 125

Val Gly Asp Asp Val Val Leu Ala Thr Gly Ser Gln Asp Phe Phe Val
 130 135 140

Arg Ser Ile Gly Ser Lys Gly Gly Lys Leu Ala Ala Gly Lys Tyr Thr
 145 150 155 160

Asp Ala Val Thr Val Thr Val Ser Asn Gln
 165 170

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- (2) INFORMATION FOR SEQ ID NO: 11:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia pestis*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TCGCCCGGGA ATTCCGAACA TAAATCGGTT CAGTGGCC

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- (2) INFORMATION FOR SEQ ID NO: 12:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia pestis*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGCGTATTCC TCGCTAGCAA TGTTTAACG

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- (2) INFORMATION FOR SEQ ID NO: 13:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO
(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Yersinia pestis*
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

ATCGTTAAAC ATTGCTAGCG AGGAATACGC C

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- (2) INFORMATION FOR SEQ ID NO: 14:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: DNA (genomic)
(iii) HYPOTHETICAL: NO
(iii) ANTI-SENSE: NO

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- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Yersinia pestis*
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GATAGATCTG TCGACTGAAC CTATTATATT GCTTCGCGC

39

- (2) INFORMATION FOR SEQ ID NO: 15:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOPTHEICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE: (A) ORGANISM: *Yersinia Pestis*
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

CTAGGAGCTC CCGCAGATTT AACTGCAAGC

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- (2) INFORMATION FOR SEQ ID NO: 16:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOPTHEICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE: (A) ORGANISM: *Yersinia Pestis*
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GATCGAGCTC GTAGGAGGTA ATATATGAAA

30

- (2) INFORMATION FOR SEQ ID NO: 17:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: DNA (genomic)
 - (iii) HYPOPTHEICAL: NO
 - (iii) ANTI-SENSE: NO
 - (vi) ORIGINAL SOURCE: (A) ORGANISM: *Yersinia Pestis*
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

CAGGTCGAGC TCGTCGACCT ATATGGATTA TTGGT

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CLAIMS.

1. Recombinant DNA that when incorporated into the DNA of a microorganism is capable of transforming that microorganism such that it is enabled to express a protein which produces a protective immune response against Yersinia pestis in a human or animal body when the microorganism is administered by oral route.
2. A plasmid capable of transforming a microorganism such that it is enabled to express a protein which produces a protective immune response against Yersinia pestis in a human or animal body when the microorganism is administered by oral route.
3. A microorganism comprising recombinant DNA, or a plasmid comprising recombinant DNA, whereby it is enabled to express a protein which produces a protective immune response against Yersinia pestis in a human or animal body when administered by oral route.
4. A microorganism as claimed in Claim 3 characterised in that it is a human or animal gut colonising microorganism.
5. Recombinant DNA, a plasmid or a microorganism as claimed in any one of claims 1 to 4 wherein the transformed microorganism maintains its ability to colonise the human or animal gut.
6. Recombinant DNA, a plasmid or a microorganism as claimed in Claim 1, 2, 3, 4 or 5 wherein the protein which produces the immune response comprises all or part of the F1 protein of Yersinia pestis.
7. Recombinant DNA comprising a DNA sequence as described in SEQ ID No 4.

8. Recombinant DNA as claimed in claim 1 comprising the F1 operon of Yersinia pestis including the caf1R, caf1M, caf1A and caf1 gene subunits.
9. Recombinant DNA as claimed in claim 8 wherein the F1 operon is derived by PCR amplification of Yersinia pestis template DNA using primer pairs of SEQ ID No 11 and 12 and SEQ ID No 13 and 14 to produce two discrete fragments, these fragments digested using NheI and then joined to provide a single F1 operon containing fragment.
10. A plasmid comprising recombinant DNA as claimed in claim 8 or 9.
11. A plasmid as claimed in claim 10 being a low copy number plasmid.
12. A plasmid as claimed in claim 10 or 11 wherein the plasmid is pLG339 or pBRD1084.
13. A plasmid as claimed in Claim 2 comprising a DNA sequence as described in SEQ ID No 4.
14. A plasmid as claimed in Claim 2 or Claim 13 characterised in that it comprises a lacZ promoter upstream of a sequence encoding for all or part of the F1 antigen.
15. A plasmid as claimed in Claim 14 characterised in that it comprises a pUC18 vector that has all or part of the caf1 sequence inserted downstream of the lacZ promoter.
16. A microorganism as claimed in Claim 3 or 4 containing recombinant DNA comprising a DNA sequence as described in SEQ ID No 4 or as claimed in claim 8 or 9.
17. A microorganism as claimed in Claim 3 or 4 containing a plasmid as claimed in any one of claims 7 to 15.

18. A microorganism as claimed in Claim 3, 4, 16 or 17 being an attenuated microorganism not capable of causing disease in humans or animals.

19. A microorganism as claimed in Claim 3, 4, 10, 11 or 12 being an aro A and/or aro C mutant.

20. A microorganism as claimed in Claim 18 or 19 being a Salmonella.

21. A microorganism as claimed in Claim 20 being a Salmonella typhimurium or a Salmonella typhi.

22. A microorganism as claimed in any one of claims 3, 4, 18, 19, 20 or 21 wherein a recombinant DNA of claim 8 or 9 is integrated directly into the microorganisms chromosomal DNA.

23. A vaccine comprising a microorganism as claimed in any one of Claim 3, 4 or 16 to 22 together with a pharmaceutically acceptable carrier.

24. A recombinant DNA, plasmid, microorganism or vaccine according to any one of claims 1 to 23 as described in Example 1 or Example 4.

Fig.1.

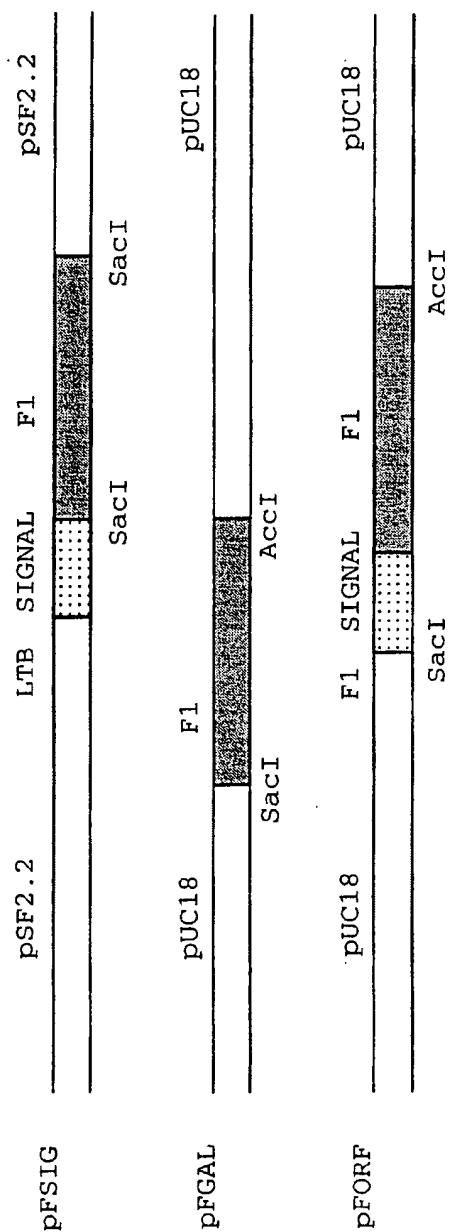
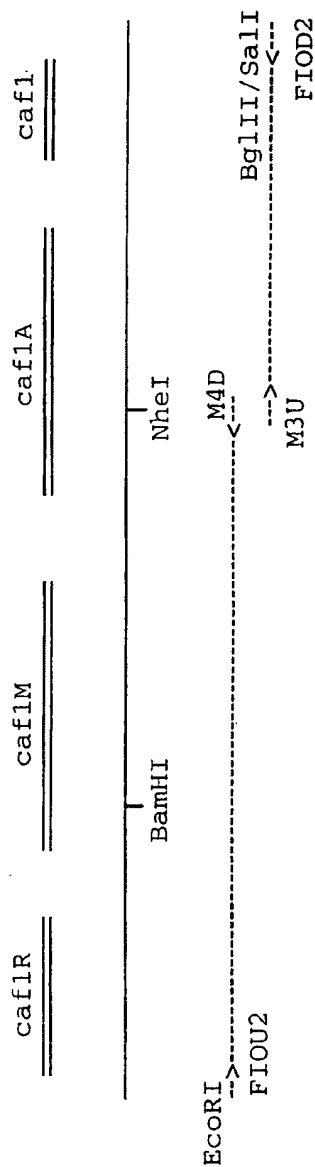


Fig.2.



INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 94/02818

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C12N15/74 C12N1/21 A61K39/02

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	AM.J.TROP.MED.HYG., vol.43, no.4, October 1990, USA pages 389 - 396 SIMPSON, W.J. ET AL. 'Recombinant capsular antigen (fraction 1) from Yersinia pestis induces a protective antibody response in Balb/C mice' cited in the application see Figure1; page 392, left-hand column, first paragraph; page 392, right-hand column, first and second paragraph --- -/--	1,2,5,6, 8-10,14, 15

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

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"E" earlier document but published on or after the international filing date

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"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

4 May 1995

Date of mailing of the international search report

29.05.95

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Authorized officer

Alt, G

INTERNATIONAL SEARCH REPORT

International Application No

PCT/GB 94/02818

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	FEBS LETTERS, vol.277, no.1,2, December 1990 pages 230 - 232 GALYOV, E.E. ET AL. 'Nucleotide sequence of the Yersinia pestis gene encoding F1 antigen and the primary structure of the protein' see page 230, right-hand column, second paragraph; Figures 1 and 2 ----	1,5,6
Y	WO,A,92 08486 (WASHINGTON UNIVERSITY) 29 May 1992 see page 12, last paragraph ----	1-24
Y	VACCINE, vol.10, no.2, 1992 pages 75 - 88 MCGHEE, J.R. ET AL. 'The mucosal immune system: From fundamental concepts to vaccine development' cited in the application see page 78, left-hand column, last paragraph; page 84, right-hand column, lines 25-65 - page 85, left-hand column, lines 1-11 ----	1-24
A	EP,A,0 474 891 (BEHRINGWERKE AKTIENGESELLSCHAFT) 18 March 1992 cited in the application ----	1
A	ADV.EXP.MED.BIOL., vol.303, 1991, USA pages 169 - 184 BREY, R.N. ET AL. 'Oral delivery of antigens in live bacterial vectors' ----	1
E	INFECTION AND IMMUNITY, vol.63, no.2, February 1995 pages 563 - 568 OYSTON, P.C.F. ET AL. 'Immunization with live recombinant Salmonella typhimurium aroA producing F1 antigen protects against plague' see whole document -----	1-24

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/GB 94/02818

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO-A-9208486	29-05-92	AU-A- 9120491	11-06-92
		CA-A- 2095534	10-05-92
		CN-A- 1063416	12-08-92
		EP-A- 0556333	25-08-93
		JP-T- 6501849	03-03-94
		NZ-A- 240538	26-01-94
		US-A- 5387744	07-02-95
		US-A- 5294441	15-03-94

EP-A-0474891	18-03-92	AU-A- 8368991	12-03-92
		CA-A- 2050876	09-03-92
		CN-A- 1060498	22-04-92

INTERNATIONAL SEARCH REPORT

International Application No

PC/GB 96/00571

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/31 C07K14/24 C12N15/62 A61K39/02

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	FEMS IMMUNOLOGY AND MEDICAL MICROBIOLOGY, 12 (3-4). 1995. 223-230., XP000573083 WILLIAMSON E D ET AL: "A new improved sub-unit vaccine for plague: The basis of protection" see the whole document	1-50
X	LEARY S E C ET AL: "Expression of Yersinia pestis V antigen in attenuated Salmonella typhimurium: Development of a novel vaccine for plague", KARGER AG, 13 (0). 1995. 216-217., BASEL, SWITZERLAND XP000572863 in Ravagnan G & Chiesa C (eds.): Yersiniosis: Present and Future. --- -/--	3,17,19

☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

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- *O* document referring to an oral disclosure, use, exhibition or other means
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T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

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Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

& document member of the same patent family

Date of the actual completion of the international search

26 June 1996

Date of mailing of the international search report

18.07.96

Name and mailing address of the ISA

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INTERNATIONAL SEARCH REPORT

Inter national Application No
PCT/GB 96/00571

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	INFECTION AND IMMUNITY, vol. 63, no. 2, February 1995, WASHINGTON US, pages 563-568, XP002006749 OYSTON P C F ET AL.: "Immunization with live recombinant Salmonella typhimurium aroA producing F1 antigen protects against plague" cited in the application see the whole document ---	3,7,19
X	INFECTION AND IMMUNITY, vol. 62, no. 10, October 1994, WASHINGTON US, pages 4192-4201, XP002006750 MOTIN V L ET AL.: "Passive immunity to Yersinia mediated by anti-recombinant V antigen and protein A-V antigen fusion peptide" see the whole document -----	3,17,19

INTERNATIONAL SEARCH REPORT

International application No.

PCT/GB96/00571

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☒ Claims Nos.: 1-14, 34-44
because they relate to subject matter not required to be searched by this Authority, namely:
Remark: Although claims 1-14, 34-44 are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.
2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.